GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 17, 2002, 01:23:59 ; Search time 86.97 Seconds
(without alignments)
2601.489 Million cell updates/sec

Title: US-09-439-311-1
Perfect score: 999
Sequence: 1 attaacacaaatgttgcagc.....ttaaaaatgatggtagagat 999

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 515962

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	26.8	2.7	30	4	US-09-358-972-102	Sequence 102, App
	2	26.8	2.7	30	4	US-09-358-972-103	Sequence 103, App
c	3	26.8	2.7	30	4	US-09-406-147-32	Sequence 32, Appl
	4	26.8	2.7	30	4	US-09-406-147-34	Sequence 34, Appl
c	5	20.8	2.1	24	1	US-08-587-209-6	Sequence 6, Appli
c	6	20.8	2.1	24	1	US-08-689-236-6	Sequence 6, Appli
c	7	20.8	2.1	24	1	US-08-689-235-6	Sequence 6, Appli
c	8	20.8	2.1	24	1	US-08-692-725-6	Sequence 6, Appli
c	9	20.8	2.1	24	2	US-08-692-726-6	Sequence 6, Appli
c	10	20.8	2.1	58	2	US-08-431-527A-7	Sequence 7, Appli
c	11	20.8	2.1	58	4	US-09-214-278-30	Sequence 30, Appl
c	12	20.6	2.1	52	3	US-08-886-967-3	Sequence 3, Appli
c	13	20.6	2.1	52	4	US-09-306-949-3	Sequence 3, Appli
c	14	20	2.0	39	3	US-08-874-825-118	Sequence 118, App
c	15	20	2.0	50	2	US-08-450-905B-7	Sequence 7, Appli
c	16	20	2.0	50	3	US-07-982-759F-7	Sequence 7, Appli
	17	20	2.0	57	1	US-08-141-892A-4	Sequence 4, Appli
	18	20	2.0	57	2	US-08-583-447A-4	Sequence 4, Appli
	19	20	2.0	57	2	US-08-467-920-4	Sequence 4, Appli
	20	20	2.0	57	3	US-08-635-930-4	Sequence 4, Appli
	21	20	2.0	57	3	US-09-193-997-4	Sequence 4, Appli
	22	20	2.0	57	4	US-09-138-237A-4	Sequence 4, Appli
	23	20	2.0	60	1	US-08-478-370-4	Sequence 4, Appli
c	24	19.6	2.0	43	1	US-07-959-946-12	Sequence 12, Appl
c	25	19.6	2.0	43	1	US-08-333-577-12	Sequence 12, Appl
c	26	19.6	2.0	43	5	PCT-US92-08634-12	Sequence 12, Appl
c	27	19.6	2.0	58	1	US-08-105-483-174	Sequence 174, App
c	28	19.6	2.0	58	1	US-08-709-209-174	Sequence 174, App
c	29	19.6	2.0	58	1	US-08-303-275-62	Sequence 62, Appl
c	30	19.6	2.0	58	1	US-08-458-101-174	Sequence 174, App
	31	19.6	2.0	60	1	US-07-670-296-19	Sequence 19, Appl
	32	19.6	2.0	60	1	US-08-093-781-20	Sequence 20, Appl
c	33	19.6	2.0	60	3	US-08-963-602-2	Sequence 2, Appli
c	34	19.4	1.9	37	2	US-08-403-853-8	Sequence 8, Appli
	35	19.4	1.9	60	1	US-08-487-890A-127	Sequence 127, App
	36	19.4	1.9	60	2	US-08-478-435-127	Sequence 127, App
	37	19.4	1.9	60	2	US-08-337-483-127	Sequence 127, App
	38	19.4	1.9	60	2	US-08-478-373-127	Sequence 127, App
	39	19.4	1.9	60	3	US-08-474-671-127	Sequence 127, App
	40	19.4	1.9	60	3	US-08-483-577A-127	Sequence 127, App
	41	19.4	1.9	60	4	US-08-897-438-127	Sequence 127, App
c	42	19.2	1.9	58	2	US-08-431-527A-6	Sequence 6, Appli
	43	19.2	1.9	60	1	US-07-609-716-72	Sequence 72, Appl
	44	19.2	1.9	60	3	US-08-475-411A-72	Sequence 72, Appl
	45	19.2	1.9	60	4	US-08-478-029A-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-09-358-972-102/c
; Sequence 102, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/358,972
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: probe to Campylobacter jejuni
US-09-358-972-102

Query Match 2.7%; Score 26.8; DB 4; Length 30;
Best Local Similarity 93.3%; Pred. No. 82;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy     289 caagatggtcaaagcttaaaaacaagaact 318
           ||||||| ||||| ||||||||||||||||
Db      30 CAAGATGGACAAAGTTTAAAAACAAGAACT 1
```

RESULT 2
US-09-358-972-103
; Sequence 103, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:

```
Qy      91 ggtcttagaatcaactccgcagca 114
           ||||||||||| ||||| ||||||
Db      24 GGTCTTAGAATTAACTCAGCAGCA 1
```

```
RESULT  13
AAV25942/c
ID   AAV25942 standard; DNA; 24 BP.
XX
AC   AAV25942;
XX
DT   15-JUL-1998  (first entry)
XX
DE   Oligonucleotide PCR primer CFO4R gene.
XX
KW   Sequence-specific; probe; enterohaemorrhagic; Escherichia coli;
KW   Salmonella; Campylobacter; Shigella; Yersinia; beta-globin;
KW   gastroenteritis; PCR primer; ss.
XX
OS   Synthetic.
OS   Campylobacter sp.
XX
PN   US5753444-A.
XX
PD   19-MAY-1998.
XX
PF   07-AUG-1996;   96US-0689235.
XX
PR   16-JAN-1996;   96US-0587209.
PR   07-AUG-1996;   96US-0689235.
XX
PA   (GULL-) GULL LAB INC.
XX
PI   Coombs J,  Glass MJ,  Malmstrom SL,  Wu L;
XX
DR   WPI; 1998-311393/27.
XX
PT   Distinguishing between similar nucleic acid samples  - using
PT   sequence-specific probes e.g. between enterohaemorrhagic and normal
PT   Escherichia coli
XX
PS   Example 3; Column 17; 21pp; English.
XX
CC   The present sequence represents a PCR primer used in an example of the
CC   present invention. The present invention describes a method for
CC   detecting mismatches between first and second nucleic acid sequences
CC   having at least one base difference. The method comprises: (a) obtaining
CC   at least one labelled probe consisting of an oligonucleotide sequence
CC   spanning the location of at least one base difference between the first
CC   and second sequences, where the oligonucleotide sequence contains at
CC   least one neutral base molecule in a position other than the position of
CC   the base difference(s) but is otherwise exactly complementary to the
CC   first sequence, so that the probe hybridises more weakly with the second
CC   sequence than with the first sequence; (b) mixing the probe(s) with the
CC   first and second sequences under hybridisation conditions; (c)
CC   dissociating any probe/second sequence hybrids; and (d) detecting
CC   probe/first sequence hybrids. The method can be used to distinguish
CC   between similar DNA/RNA sequences in a sample, especially to distinguish
CC   enterohaemorrhagic E. coli O157:H7 from other E. coli strains e.g. in
CC   stool samples from people suffering from gastroenteritis, caused
CC   specifically by enterohaemorrhagic E.coli. Use of the method shortens
CC   the time between sample preparation to obtaining results, than has been
CC   possible with previous similar procedures.
XX
SQ   Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 other;
```

```
  Query Match             2.1%;  Score 20.8;  DB 19;  Length 24;
  Best Local Similarity   91.7%;  Pred. No. 3.4e+04;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      91 ggtcttagaatcaactccgcagca 114
           ||||||||||| ||||| ||||||
Db      24 GGTCTTAGAATTAACTCAGCAGCA 1
```

```
RESULT  14
AAV20847/c
ID   AAV20847 standard; DNA; 24 BP.
XX
AC   AAV20847;
XX
DT   01-JUL-1998  (first entry)
XX
DE   Campylobacter CFO4R gene PCR primer.
XX
KW   Escherichia coli strain O157:H7; detection; microorganism; infection;
KW   enterohaemorrhagic; PCR primer; ss.
XX
OS   Synthetic.
OS   Campylobacter sp.
XX
PN   US5738995-A.
XX
PD   14-APR-1998.
XX
PF   07-AUG-1996;   96US-0689236.
XX
PR   16-JAN-1996;   96US-0587209.
PR   07-AUG-1996;   96US-0689236.
XX
PA   (GULL-) GULL LAB INC.
XX
PI   Coombs J,  Glass MJ,  Malmstrom SL,  Wu L;
XX
DR   WPI; 1998-260031/23.
XX
PT   Probes for detecting Escherichia coli strain O157:H7 - useful for
PT   diagnosis of enterohaemorrhagic Escherichia coli infection(s)
XX
PS   Example 3; Column 17; 21pp; English.
XX
CC   The present sequence represents a PCR primer used in an example of the
CC   present invention. The present invention describes probes used in the
CC   detection of Escherichia coli strain O157:H7 in a sample. The method of
CC   detection comprises: (a) obtaining at least 1 probe specifically given
CC   in the specification, labelled with a label that permits probe detection
CC   when hybridised to a complementary nucleic acid sequence which is
CC   specific for a nucleic acid sequence of the microorganism; (b)
CC   hybridising the probes and the sample, and (c) detecting hybrids
CC   comprising the probes and the nucleic acid sequences. The method and
CC   probes may be used for diagnosis of enterohaemorrhagic E. coli
CC   infections. The methods and the materials permit the detection and
CC   discrimination of multiple analytes.
XX
SQ   Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 other;
```

```
  Query Match             2.1%;  Score 20.8;  DB 19;  Length 24;
  Best Local Similarity   91.7%;  Pred. No. 3.4e+04;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      91 ggtcttagaatcaactccgcagca 114
           ||||||||||| ||||| ||||||
Db      24 GGTCTTAGAATTAACTCAGCAGCA 1
```

```
RESULT  15
AAF16711
ID   AAF16711 standard; DNA; 44 BP.
XX
AC   AAF16711;
XX
DT   09-MAR-2001  (first entry)
XX
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AAA97417
ID   AAA97417 standard; DNA; 54 BP.
XX
AC   AAA97417;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Pea wild-type pra2 gene light-repressible promoter oligonucleotide, WT3.
XX
KW   GTP-binding protein pra2; pea; light-repressible promoter;
KW   photoinhibitory; expression cassette; transgenic plant;
KW   deterioration prevention; storage; ss.
XX
OS   Pisum sativum.
XX
PN   WO200055313-A1.
XX
PD   21-SEP-2000.
XX
PF   03-MAR-2000; 2000WO-JP01269.
XX
PR   12-MAR-1999;   99JP-0066551.
XX
PA   (SUNR ) SUNTORY LTD.
XX
PI   Sasaki Y,  Nagano Y,  Inaba T;
XX
DR   WPI; 2000-587526/55.
XX
PT   New DNA fragment or promoter for expressing a target gene, specifically
PT   under photoinhibitory conditions, and for transforming a plant cell or
PT   plant to improve quality and prevent deterioration during storage
XX
PS   Example 9; Page 19; 49pp; Japanese.
XX
CC   The invention relates to a light-repressible promoter (AAA97385), or
CC   active fragments thereof (AAA97383, AAA97384), from the gene encoding
CC   the pea GTP-binding protein pra2. The invention also relates to an
CC   expression cassette containing the pra2 promoter or its active
CC   fragments for the expression of a gene under photoinhibitory or dark
CC   conditions in a plant, and to transgenic plants, their descendants
CC   and plant tissues comprising the expression cassette. The expression
CC   cassette of the invention can be used to generate transgenic plants in
CC   which deterioration during storage in the dark is prevented. This is
CC   particularly useful for agricultural products. Sequences AAA97417-A97418
CC   represent oligonucleotides used in an exemplification of the invention
CC   to generate a wild-type pea pra2 promoter fragment.
XX
SQ   Sequence 54 BP; 18 A; 3 C; 12 G; 21 T; 0 other;


  Query Match             2.1%;  Score 21.2;  DB 21;  Length 54;
  Best Local Similarity  64.0%;  Pred. No. 3.3e+04;
  Matches   32;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy    738 tcaggattttgctatcaatggggttgttataggtaaggttgattattcag 787
          | |||||||| |  | | || || | ||| ||  |  |  |||| | |||
Db      1 tgaggattttacagtaattgaggattttacagtaattgaggattttacag 50


RESULT  9
AAA27148
ID   AAA27148 standard; DNA; 27 BP.
XX
AC   AAA27148;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Campylobacter coli flaA gene primer flaA-11.
XX
KW   Flagellin; flaA; diarrhoea; Guillain-Barre syndrome;
KW   vaccine; GBS; PCR primer; ss.
XX
OS   Campylobacter coli.
XX
PN   WO200027205-A1.
XX
PD   18-MAY-2000.
XX
PF   12-NOV-1999;   99WO-US27195.
XX
PR   12-NOV-1998;   98US-0108114.
XX
PA   (USAT ) US SEC.
XX
PI   Guerry P,  Trust T,  Burg E,  Lee L;
XX
DR   WPI; 2000-376214/32.
XX
PT   Campylobacter FlaA protein and coding sequence, useful in reducing
PT   Campylobacter intestinal colonization
XX
PS   Disclosure; Page 7; 43pp; English.
XX
CC   The flaA gene encodes the major flagellin subunit of the Campylobacter
CC   coli flagellar filament. Part of the FlaA polypeptide may be fused with
CC   the maltose binding protein of Escherichia coli to make a recombinant
CC   protein. When this protein is introduced into a host an immunological
CC   response is triggered. Therefore the recombinant protein may be used as
CC   a vaccine to protect against C. coli intestinal colonisation and the
CC   diarrhoea it causes. This vaccine system is useful as it can
CC   prevent the development of Guillain-Barre syndrome (GBS) which is seen
CC   with whole cell Campylobacter vaccines. The present sequence is the
CC   flaA-11 PCR primer that was used to amplify part of the flaA gene.
XX
SQ   Sequence 27 BP; 12 A; 6 C; 3 G; 6 T; 0 other;


  Query Match             2.1%;  Score 21;  DB 21;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+04;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 attaacacaaatgttgcagca 21
          |||||||||||||||||||||
Db      7 attaacacaaatgttgcagca 27


RESULT  10
AAA27149/c
ID   AAA27149 standard; DNA; 33 BP.
XX
AC   AAA27149;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Campylobacter coli flaA gene primer flaA-2.
XX
KW   Flagellin; flaA; diarrhoea; Guillain-Barre syndrome;
KW   vaccine; GBS; PCR primer; ss.
XX
OS   Campylobacter coli.
XX
PN   WO200027205-A1.
XX
PD   18-MAY-2000.
XX
PF   12-NOV-1999;   99WO-US27195.
XX
PR   12-NOV-1998;   98US-0108114.
XX
PA   (USAT ) US SEC.
XX
PI   Guerry P,  Trust T,  Burg E,  Lee L;
XX
DR   WPI; 2000-376214/32.
XX
```